



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 12:43 PM EDT

PDB ID : 6N8L
EMDB ID : EMD-0371
Title : Cryo-EM structure of early cytoplasmic-late (ECL) pre-60S ribosomal subunit
Authors : Zhou, Y.; Musalgaonkar, S.; Johnson, A.W.; Taylor, D.W.
Deposited on : 2018-11-29
Resolution : 3.60 Å(reported)
Based on initial model : 3JCT

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

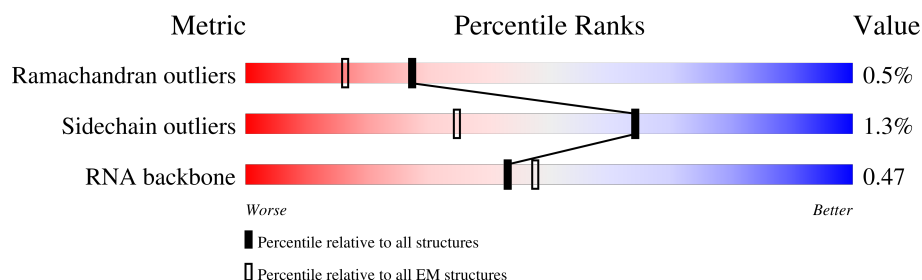
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



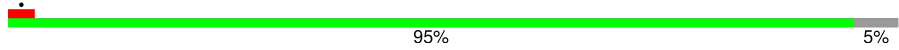

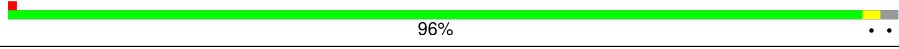

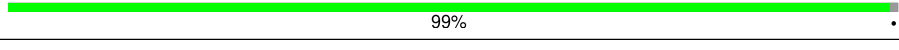

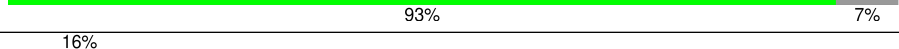
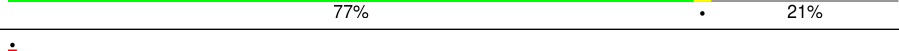
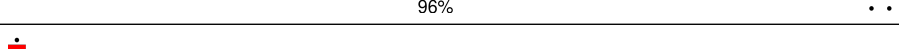
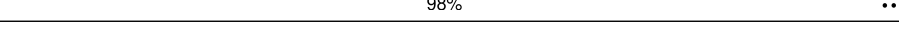
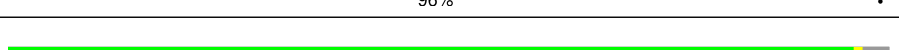
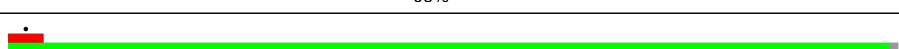
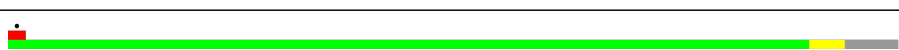
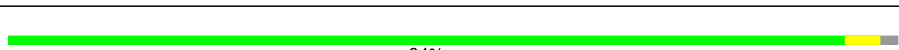
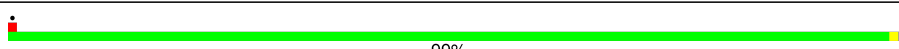
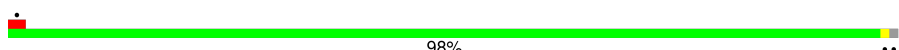
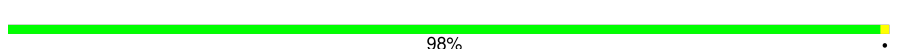

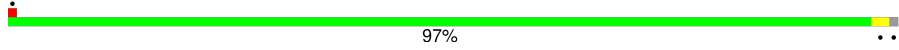
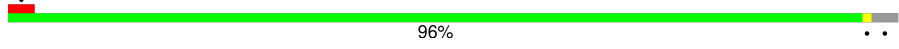
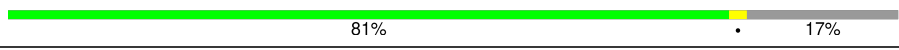
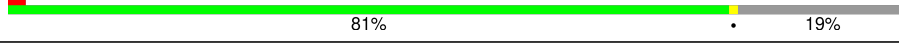
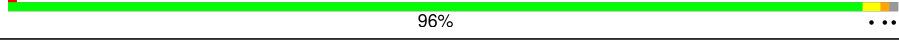


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	v	518	
2	s	217	
3	A	254	
4	a	149	
5	B	387	
6	b	647	
7	C	362	
8	c	105	

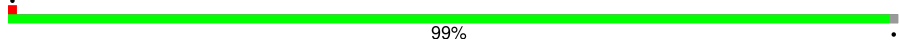
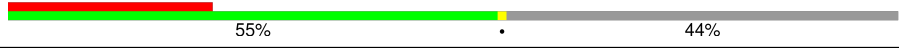

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	d	113	
10	E	176	
11	e	130	
12	F	244	
13	f	107	
14	G	256	
15	g	121	
16	I	166	
17	H	191	
18	h	120	
19	i	100	
20	j	88	
21	k	78	
22	L	199	
23	l	51	
24	M	138	
25	p	92	
26	N	204	
27	u	199	
28	O	199	
29	P	184	
30	Q	186	
31	R	189	
32	S	172	
33	T	160	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	U	121	
35	V	137	
36	W	236	
37	X	142	
38	Y	127	
39	y	245	
40	Z	136	
41	z	106	
42	D	297	
43	J	174	
44	q	106	
45	o	59	
46	1	3396	
47	2	121	
48	3	158	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 129926 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	v	362	Total	C	N	O	S	0	0
			2783	1770	472	522	19		

- Molecule 2 is a protein called Ribosomal Protein uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	s	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	245	Total	C	N	O	S	0	0
			1863	1162	376	324	1		

- Molecule 4 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	94	Total	C	N	O	S	0	0
			742	484	131	126	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 6 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	248	Total	C	N	O	S	0	0
			1989	1222	372	387	8		

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 8 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 9 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	160	Total	C	N	O	S	0	0
			1270	818	229	222	1		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 13 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 15 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 16 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	131	Total	C	N	O	S	0	0
			1056	660	195	198	3		

- Molecule 17 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 18 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 19 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 20 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 21 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 22 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	L	187	Total	C	N	O	0	0
			1491	929	306	256		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 24 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 25 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 26 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 27 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	u	149	Total	C	N	O	S	0	0
			1256	788	252	207	9		

- Molecule 28 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 29 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P	178	Total	C	N	O		0	0
			1409	876	281	252			

- Molecule 30 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Q	154	Total	C	N	O	S	0	0
			1191	753	231	205	2		

- Molecule 31 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	R	154	Total	C	N	O		0	0
			1241	772	262	207			

- Molecule 32 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S	170	Total	C	N	O	S	0	0
			1425	916	265	241	3		

- Molecule 33 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	61	Total	C	N	O	S	0	0
			476	295	95	85	1		

- Molecule 34 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	U	104	Total	C	N	O		0	0
			826	535	136	155			

- Molecule 35 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 36 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	W	133	Total	C	N	O	S	0	0
			1053	660	177	214	2		

- Molecule 37 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 38 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	y	225	Total	C	N	O	S	0	0
			1698	1054	295	343	6		

- Molecule 40 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 41 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	z	55	Total	C	N	O		0	0
			444	273	88	83			

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	D	251	Total	C	N	O	S	0	0
			1983	1253	353	375	2		

- Molecule 43 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	J	164	Total	C	N	O	S	0	0
			1304	816	243	242	3		

- Molecule 44 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	97	Total	C	N	O	S	0	0
			783	493	158	127	5		

- Molecule 45 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	o	54	Total	C	N	O	0	0
			433	271	94	68		

- Molecule 46 is a RNA chain called *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	3201	Total	C	N	O	P	0	0
			68471	30584	12345	22341	3201		

- Molecule 47 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

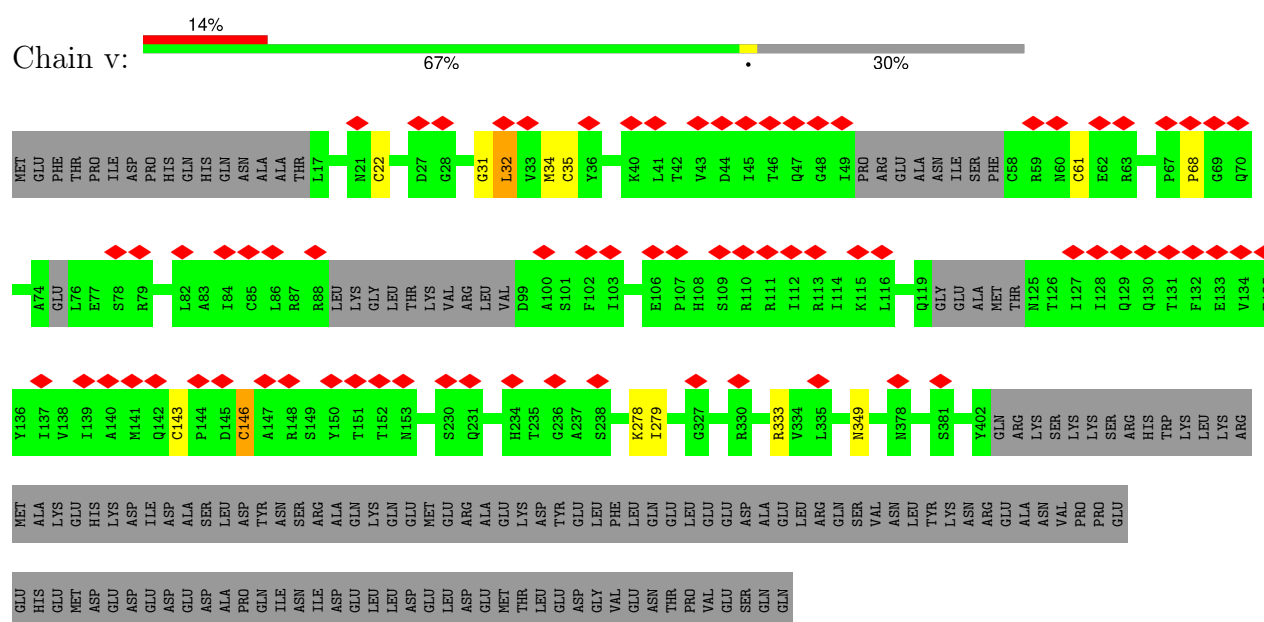
- Molecule 48 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	3	157	Total	C	N	O	P	0	0
			3333	1491	584	1101	157		

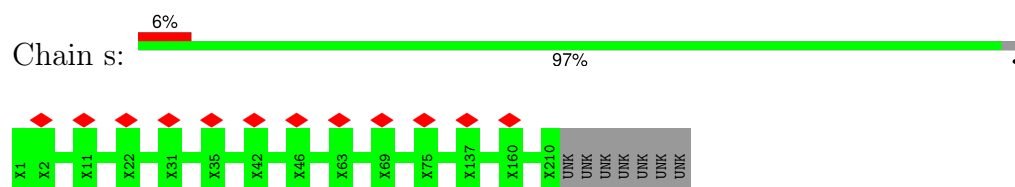
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

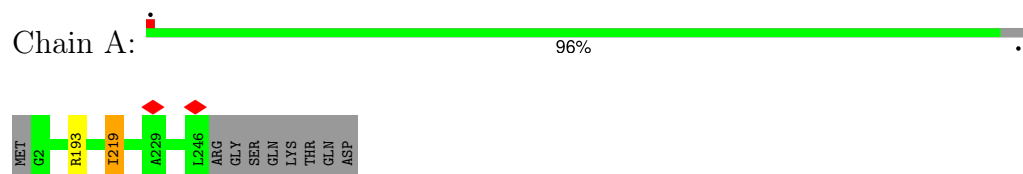
- Molecule 1: 60S ribosomal export protein NMD3



- Molecule 2: Ribosomal Protein uL1

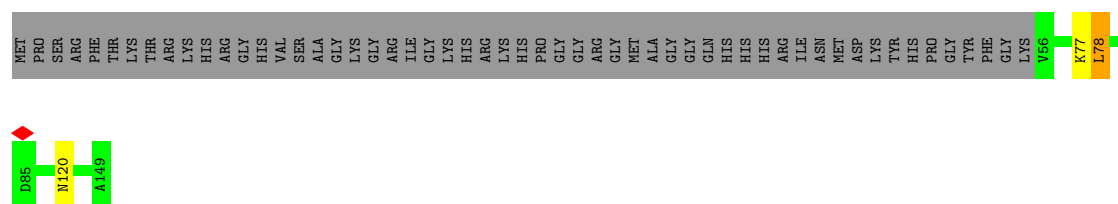


- Molecule 3: 60S ribosomal protein L2-A



- Molecule 4: 60S ribosomal protein L28

Chain a: 



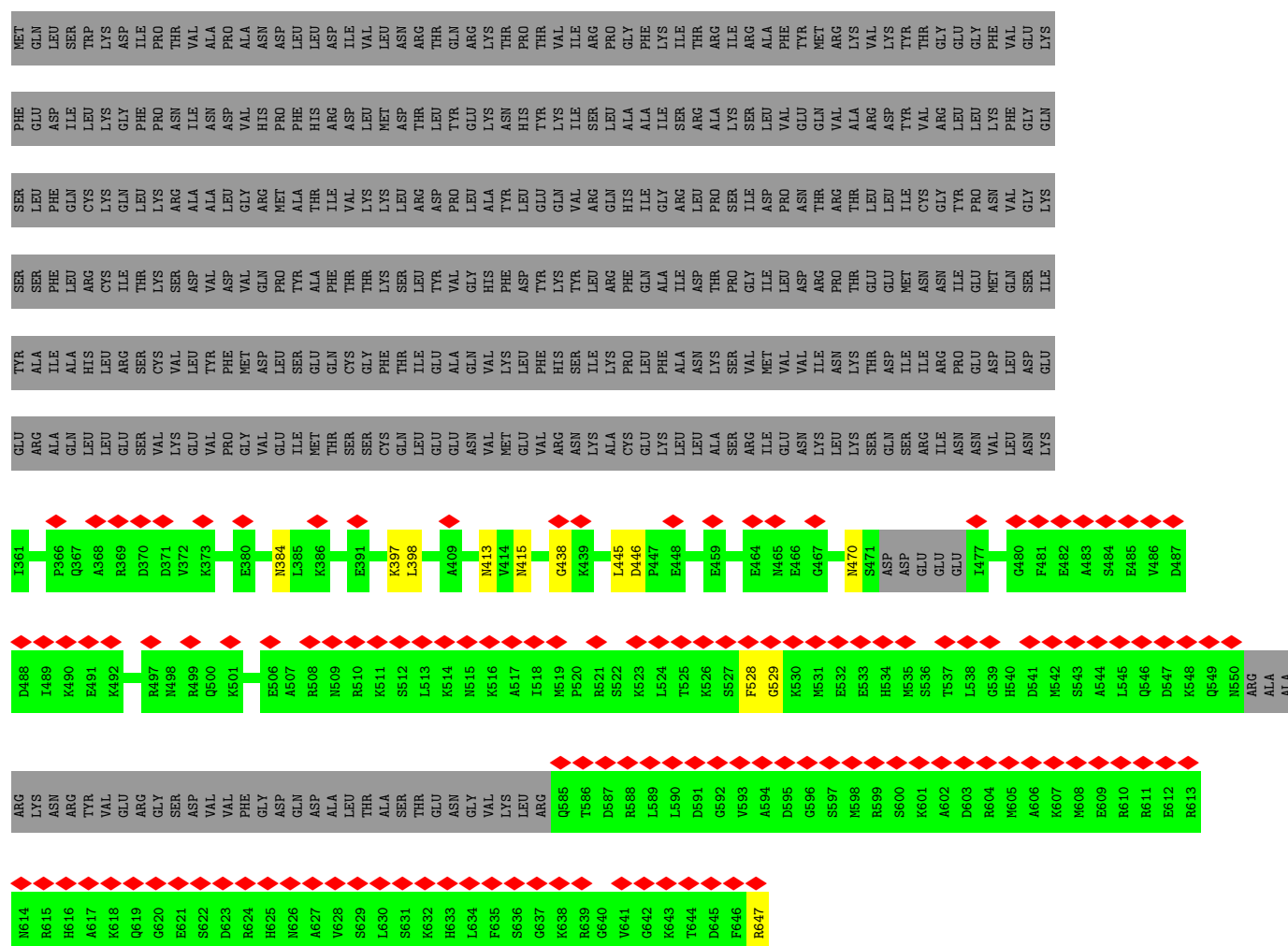
- Molecule 5: 60S ribosomal protein L3

Chain B: 



- Molecule 6: Nucleolar GTP-binding protein 1

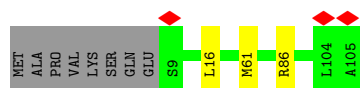
Chain b: 



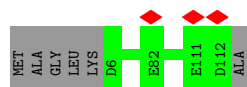
- Molecule 7: 60S ribosomal protein L4-A



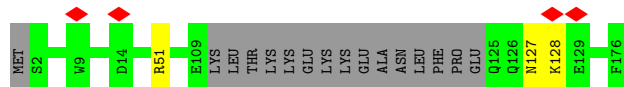
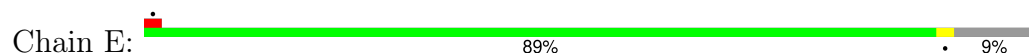
- Molecule 8: 60S ribosomal protein L30



- Molecule 9: 60S ribosomal protein L31-A



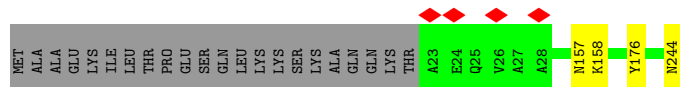
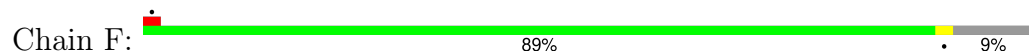
- Molecule 10: 60S ribosomal protein L6-A



- Molecule 11: 60S ribosomal protein L32




- Molecule 12: 60S ribosomal protein L7-A



- Molecule 13: 60S ribosomal protein L33-A




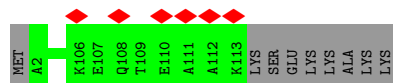
- Molecule 14: 60S ribosomal protein L8-A

Chain G:  87% 10%




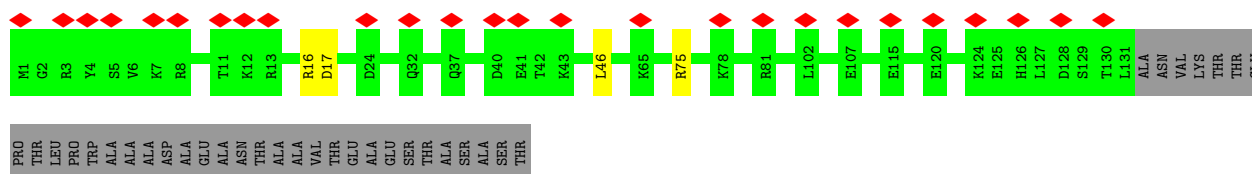
- Molecule 15: 60S ribosomal protein L34-A

Chain g:  5% 93% 7%



- Molecule 16: Bud site selection protein 20

Chain I:  16% 77% 21%



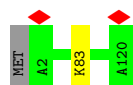
- Molecule 17: 60S ribosomal protein L9-A

Chain H:  96%



- Molecule 18: 60S ribosomal protein L35-A

Chain h:  98%



- Molecule 19: 60S ribosomal protein L36-A

Chain i:  96%

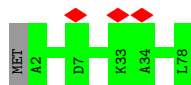


- Molecule 20: 60S ribosomal protein L37-A

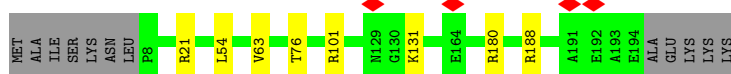
Chain j:  95%



- Molecule 21: 60S ribosomal protein L38



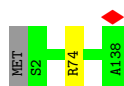
- Molecule 22: 60S ribosomal protein L13-A



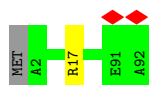
- Molecule 23: 60S ribosomal protein L39



- Molecule 24: 60S ribosomal protein L14-A



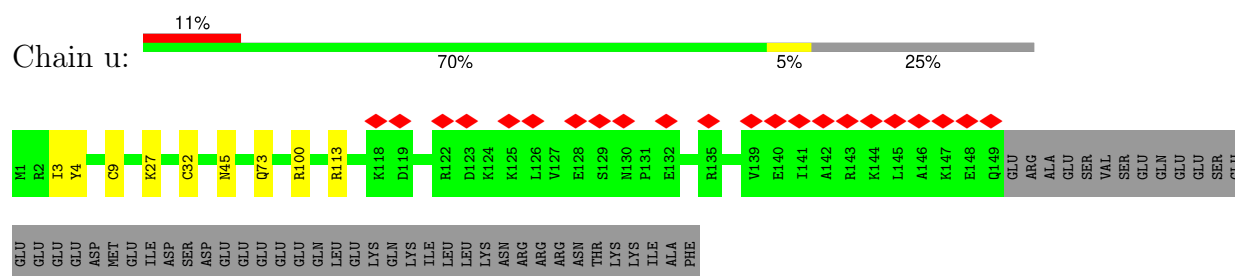
- Molecule 25: 60S ribosomal protein L43-A



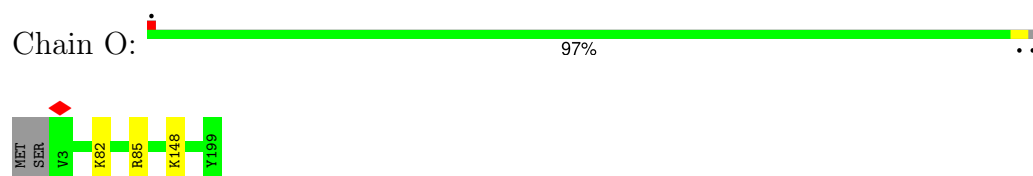
- Molecule 26: 60S ribosomal protein L15-A



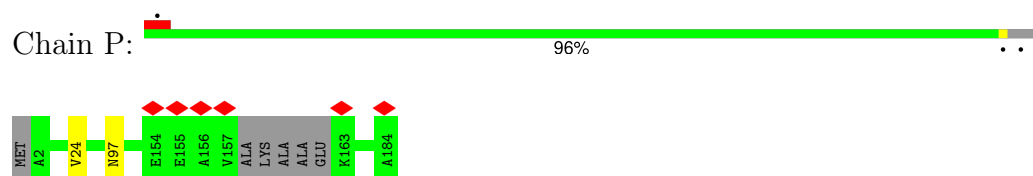
- Molecule 27: Ribosome biogenesis protein RLP24



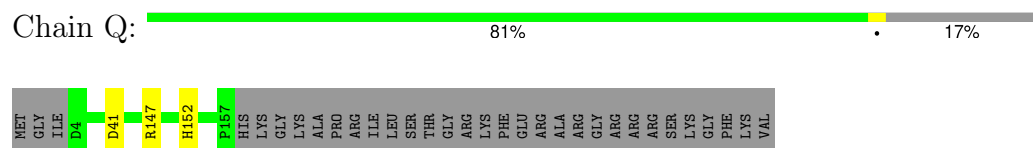
- Molecule 28: 60S ribosomal protein L16-A



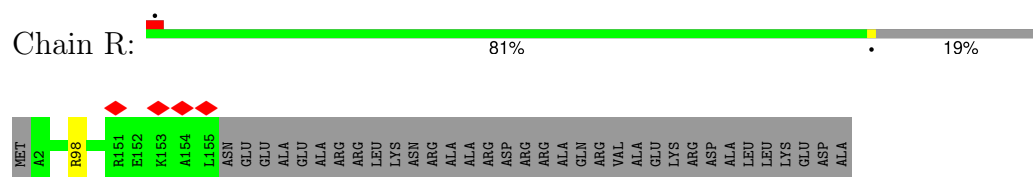
- Molecule 29: 60S ribosomal protein L17-A



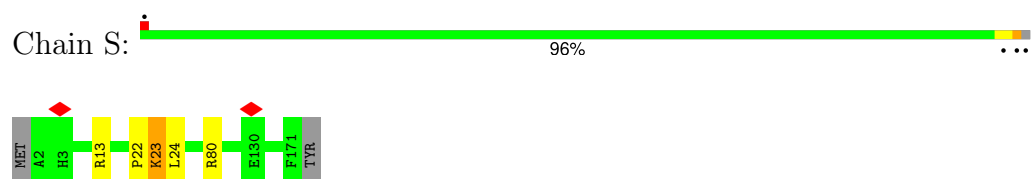
- Molecule 30: 60S ribosomal protein L18-A



- Molecule 31: 60S ribosomal protein L19-A



- Molecule 32: 60S ribosomal protein L20-A




- Molecule 33: 60S ribosomal protein L21-A



MET GLY LYS SER HIS GLY TYR ARG SER ARG THR ARG THR MET PHE GLN ARG ASP PHE ARG LYS LYS HIS GLY ASP ASP ILE VAL ASP ILE LYS ALA ASN GLY SER ILE GLN LYS PHE GLY MET PRO HIS LYS PHE TYR GLN GLY LYS

THR GLY VAL VAL TYR ASN VAL THR LYS SER SER VAL GLY VAL ILE ILE ASN LYS LYS MET VAL GLY LYS HIS VAL ARG ASP TYR VAL LEU LEU LYS LYS ARG LEU LEU VAL VAL TYR LYS HIS VAL GLY ASP ASP ILE VAL ASP ILE LYS ALA ASN GLY SER ILE GLN LYS PHE GLY MET PRO HIS LYS PHE TYR GLN GLY LYS

• Molecule 34: 60S ribosomal protein L22-A

Chain U:  84% 14%

MET ALA PRO ASN THR SER ARG LYS Q9 K49 R94 Q109 V110 T111 F112 GLU GLU ASP GLU GLU GLU ASP GLU

• Molecule 35: 60S ribosomal protein L23-A

Chain V:  99%

MET S2 G3 V137

• Molecule 36: Ribosome assembly factor MRT4

Chain W:  23% 55% 44%


MET PRO ARG SER LYS ARG SER LYS LEU VAL THR LEU ALA GLN THR ASP LYS LYS G19 N22 D28 E29 E32 A33 L34 D35 T36 Y37 V42 L43 H44 L45 D46 D47 T58 A61 G62 S63 K64 K69 R70 K71 V72 L73 A76 E83 E84 Y85 K86 E87 N88

L89 Y90 Q91 L92 S93 K94 L95 C96 D106 E107 D108 V109 M110 T111 E114 Y115 F116 K117 S118 R121 S122 D123 R126 PRO ASN THR LYS LYS ALA PRO LEU THR PHE THR ILE ILE LEU LYS GLN GLY ILE VAL TYR SER ARG GLY GLY GLN K71 ILE ILE PRO ALA GLU GLU ASP VAL PRO MET ILE HIS

SER LEU PRO THR MET ARG ASN PHE LEU ILE PRO THR LYS ILE LYS ALA GLY LYS ILE THR ASP SER PRO TYR LEU VAL CYS THR GLY GLU GLU ASN THR LYS LEU ASP VAL ARG GLN ALA LEU LEU ILE LEU LYS GLN PHE GLY ILE ILE ALA A210 S211 E212 F213 K214 V217 S218 A219

D224 S225 E229 N232 I233 N234 MET GLU

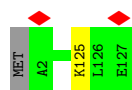
• Molecule 37: 60S ribosomal protein L25

Chain X:  84% 15%

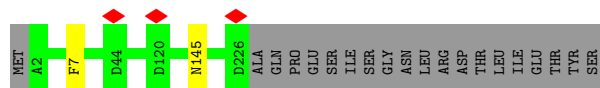
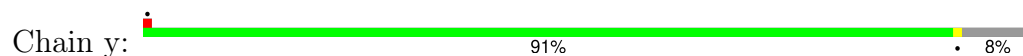
MET ALA PRO PRO ALA LYS ALA THR ALA ALA LYS LYS ALA VAL VAL LYS GLY THR ASN GLY A23 M73 D78 F142

• Molecule 38: 60S ribosomal protein L26-A

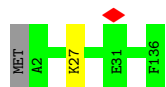
Chain Y:  98%



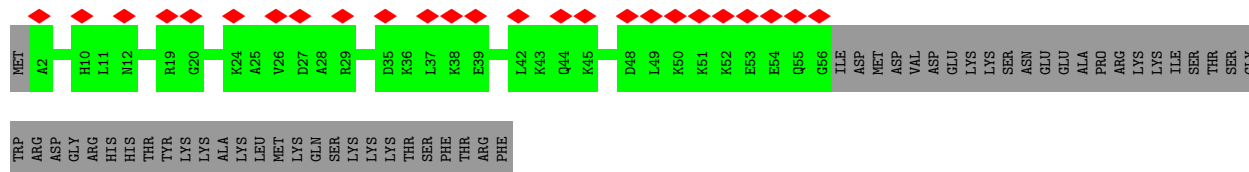
- Molecule 39: Eukaryotic translation initiation factor 6



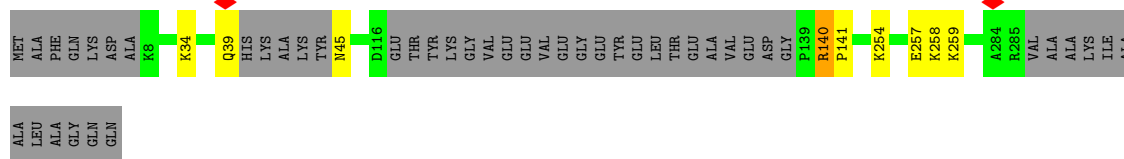
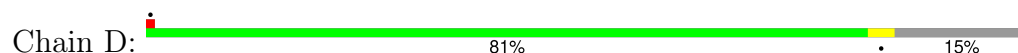
- Molecule 40: 60S ribosomal protein L27-A



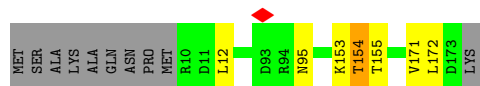
- Molecule 41: UPF0642 protein YBL028C



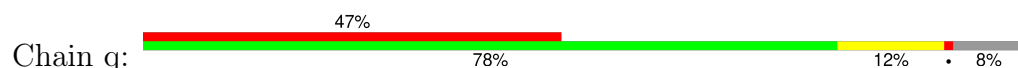
- Molecule 42: 60S ribosomal protein L5

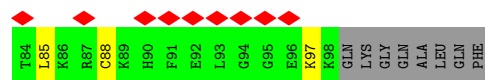


- Molecule 43: 60S ribosomal protein L11-A

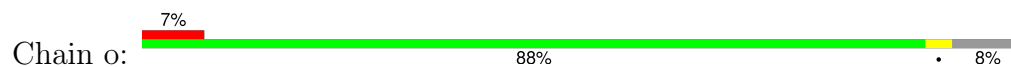


- Molecule 44: 60S ribosomal protein L42-A

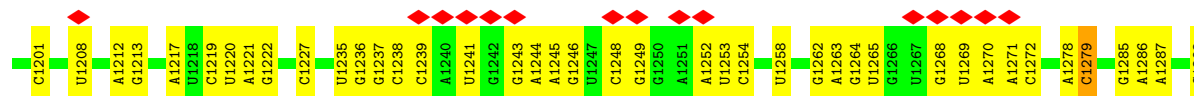
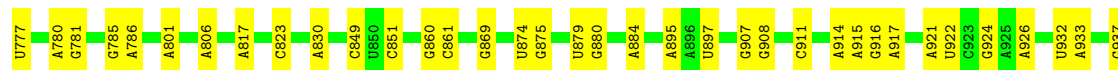
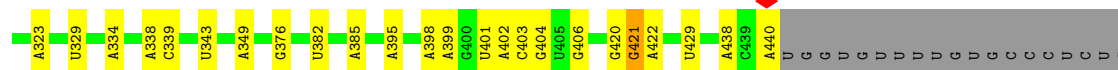




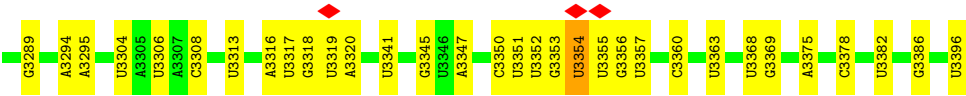
- Molecule 45: 60S ribosomal protein L29



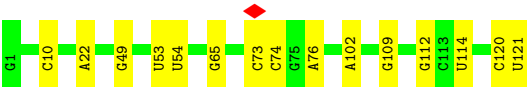
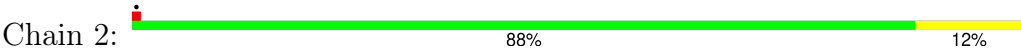
- Molecule 46: *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA



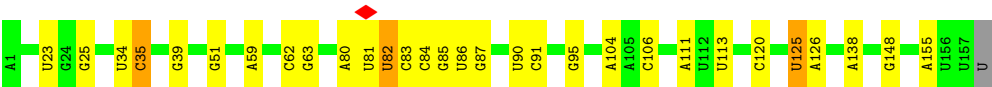
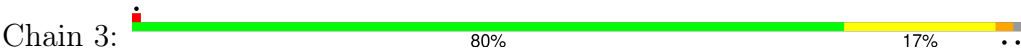
C3164	A2934	G2810	G2848	U2508	A2401	A	U	G	A1588	A1475	G1295
A3165	U2935	C2814	U2652	U2513	A2402	A	A	C	A1589	G1480	G1305
A3168	A2936	G2815	U2652	U2514	G2403	C	C	U	G1590	A1481	U1305
U3170	A2941	G2816	A2656	G2522	G2404	A	A	G	A1593	G1482	G1306
G3173	G2951	A2817	A2657	G2522	U2411	U	U	C	A1619	G1483	G1307
A3174	A2971	U2818	A2674	C2531	U2411	A	A	C	U1620	U1484	A1308
U3175	U2978	A2819	G2677	U2532	G2435				G1492		U1309
G3176	U2978	A2820	A2678	G2533	U2436				C1496		G1313
U3179	C2983	C2821	A2678	U2537	G2437				C1316		
A3180	C2983	G2828	U2688	U2538	G2440				A1503		C1320
C3181	U2996	A2838	A2688	C2539	A2441				C1508		U1325
A3187	G2997	C2836	A2689	A2540	G2442				U1512		A1330
U3196	A3011	U2837	A2691	U2541					U1512		U1331
U3207	A3012	A2838	A2694	U2542	G2448				A1537		A1332
G3208	A3021	A2843	A2695	U2543	A2449				A1546		U1348
A3209	A3028	C2844	A2696	U2544	G2450				G1547		A1350
A3210	U3056	A2845	A2703	A2547	G2451				U1554		U1351
U3214	U3059	U2846	A2704	C2548	G2452				C1556		A1352
C3217	G3080	C2851	A2705	G2549	U2453				A1557		U1353
G3219	A3086	A2851	A2719	U2550	U2455				U1558		A1355
C3228	C3092	C2852	C2726	U2551	A2458				A1566		U1356
G3229	C3099	U2860	U2727	C2552	A2459				A1567		A1366
G3239	G3108	U2861	G2753	U2553	U2460				C1569		C1391
A3242	G3109	U2862	G2754	C2558	U2471				G1580		G1392
A3243	U2863	G2863	G2755	U2570	U2472				G1581		A1399
A3244	A2864	U2864	C2755	U2571	G2473				C1582		G1400
G3246	U2865	U2865	A2762	U2572	G2474				U1564		U1408
G3247	U2866	U2866	A2768	G2573	G2475				C1416		C1416
U3259	U3119	C2867	A2769	C2577	G2476				U1567		U1567
G3260	A3129	U2868	G2770	G2585	G2477				U1568		U1568
G3263	U3131	U2869	U2771	C2585	A2484				U1569		A1419
C3265	A3142	C2870	C2772	A2593	A2485				U1570		U1430
A3268	C3143	G2871	G2777	C2594	U2487				A1571		G1434
U3270	U3148	U2875	G2778	C2600	C2495				U1572		G1443
U3275	G3149	C2876	G2794	G2606	C2496				G1573		G1444
G3276	A3150	A2887	G2796	G2607	U2497				C1574		U1445
U3279	C2889	C2889	A2799	U2614	U2499				A1575		A1446
A3279	U2904	U2890	G2800	U2617	U2501				G1576		G1443
U3280	U3155	A2801	A2801	U2617	A2502				G1577		C1578
U3157	U3156	A2802	A2802	U2617	G2503				C1579		A1580
		A2803	A2803	U2617	U2504				C1581		C1582
		U2923	U2923	U2617	U2505				U1763		U1455
		U2924	U2924	U2617	U2506				U1764		
		C2928	C2928	U2617	C2507						
		A2933	A2933	U2617							



• Molecule 47: 5S rRNA



• Molecule 48: 5.8S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42030	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.145	Depositor
Minimum map value	-0.077	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	v	0.40	0/2831	0.68	4/3847 (0.1%)
3	A	0.46	0/1897	0.65	0/2550
4	a	0.43	0/758	0.53	0/1023
5	B	0.47	0/3152	0.66	1/4239 (0.0%)
6	b	0.30	0/2016	0.59	0/2692
7	C	0.41	0/2801	0.60	0/3792
8	c	0.41	0/751	0.56	0/1008
9	d	0.44	0/887	0.58	0/1191
10	E	0.37	0/1291	0.57	0/1735
11	e	0.39	0/1041	0.55	0/1394
12	F	0.42	0/1821	0.60	2/2451 (0.1%)
13	f	0.48	0/868	0.53	0/1168
14	G	0.41	0/1830	0.64	1/2469 (0.0%)
15	g	0.44	0/891	0.59	0/1191
16	I	0.31	0/1072	0.58	1/1440 (0.1%)
17	H	0.38	0/1514	0.57	1/2039 (0.0%)
18	h	0.36	0/978	0.56	0/1301
19	i	0.36	0/749	0.58	0/995
20	j	0.45	0/685	0.62	0/908
21	k	0.37	0/618	0.56	0/826
22	L	0.41	0/1516	0.62	0/2037
23	l	0.40	0/443	0.60	0/588
24	M	0.38	0/1074	0.53	0/1446
25	p	0.43	0/701	0.58	0/934
26	N	0.49	0/1757	0.60	1/2354 (0.0%)
27	u	0.39	0/1278	0.62	2/1699 (0.1%)
28	O	0.42	0/1585	0.54	0/2128
29	P	0.43	0/1431	0.56	0/1921
30	Q	0.40	0/1211	0.65	1/1633 (0.1%)
31	R	0.41	0/1258	0.59	0/1679
32	S	0.42	0/1460	0.58	0/1962
33	T	0.33	0/483	0.55	0/650
34	U	0.34	0/843	0.58	0/1143
35	V	0.43	0/1018	0.60	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	W	0.28	0/1068	0.55	1/1442 (0.1%)
37	X	0.42	0/974	0.57	0/1314
38	Y	0.38	0/1004	0.57	0/1341
39	y	0.34	0/1719	0.57	0/2340
40	Z	0.42	0/1118	0.58	0/1497
41	z	0.25	0/445	0.43	0/585
42	D	0.38	0/2023	0.58	0/2729
43	J	0.31	0/1324	0.60	0/1778
44	q	0.50	1/795 (0.1%)	0.93	4/1050 (0.4%)
45	o	0.38	0/444	0.55	0/592
46	1	0.76	1/76644 (0.0%)	0.97	150/119495 (0.1%)
47	2	0.64	0/2883	0.88	0/4491
48	3	0.80	0/3724	0.94	5/5798 (0.1%)
All	All	0.64	2/138674 (0.0%)	0.85	174/204254 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	v	0	3
3	A	0	1
5	B	0	3
6	b	0	3
7	C	0	1
12	F	0	1
14	G	0	2
16	I	0	1
17	H	0	1
18	h	0	1
22	L	0	1
30	Q	0	1
32	S	0	2
33	T	0	1
38	Y	0	1
39	y	0	2
42	D	0	3
43	J	0	3
44	q	0	9
45	o	0	1
All	All	0	41

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	1	2971	A	N9-C4	5.09	1.41	1.37
44	q	69	VAL	CB-CG1	-5.04	1.42	1.52

The worst 5 of 174 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	1	3217	C	N1-C2-O2	11.81	125.99	118.90
30	Q	41	ASP	CB-CG-OD1	9.70	127.03	118.30
46	1	3217	C	C2-N1-C1'	9.70	129.47	118.80
46	1	3217	C	N3-C2-O2	-9.02	115.59	121.90
1	v	146	CYS	CA-CB-SG	8.84	129.91	114.00

There are no chirality outliers.

5 of 41 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	219	ILE	Peptide
5	B	33	PRO	Peptide
1	v	278	LYS	Peptide
1	v	31	GLY	Peptide
1	v	32	LEU	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	v	352/518 (68%)	305 (87%)	44 (12%)	3 (1%)	14 48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	243/254 (96%)	217 (89%)	25 (10%)	1 (0%)	30	63
4	a	92/149 (62%)	84 (91%)	6 (6%)	2 (2%)	5	32
5	B	384/387 (99%)	343 (89%)	38 (10%)	3 (1%)	16	51
6	b	242/647 (37%)	226 (93%)	13 (5%)	3 (1%)	11	43
7	C	359/362 (99%)	325 (90%)	31 (9%)	3 (1%)	16	51
8	c	95/105 (90%)	91 (96%)	4 (4%)	0	100	100
9	d	105/113 (93%)	100 (95%)	5 (5%)	0	100	100
10	E	156/176 (89%)	148 (95%)	8 (5%)	0	100	100
11	e	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
12	F	220/244 (90%)	197 (90%)	23 (10%)	0	100	100
13	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
14	G	228/256 (89%)	209 (92%)	19 (8%)	0	100	100
15	g	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
16	I	129/166 (78%)	116 (90%)	12 (9%)	1 (1%)	16	51
17	H	186/191 (97%)	168 (90%)	18 (10%)	0	100	100
18	h	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
19	i	94/100 (94%)	87 (93%)	7 (7%)	0	100	100
20	j	83/88 (94%)	76 (92%)	7 (8%)	0	100	100
21	k	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
22	L	185/199 (93%)	163 (88%)	21 (11%)	1 (0%)	25	59
23	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
24	M	135/138 (98%)	128 (95%)	7 (5%)	0	100	100
25	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
26	N	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
27	u	147/199 (74%)	137 (93%)	7 (5%)	3 (2%)	6	34
28	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
29	P	174/184 (95%)	169 (97%)	5 (3%)	0	100	100
30	Q	152/186 (82%)	141 (93%)	11 (7%)	0	100	100
31	R	152/189 (80%)	145 (95%)	7 (5%)	0	100	100
32	S	168/172 (98%)	149 (89%)	16 (10%)	3 (2%)	7	35
33	T	59/160 (37%)	54 (92%)	5 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	U	102/121 (84%)	94 (92%)	8 (8%)	0	100	100
35	V	134/137 (98%)	129 (96%)	5 (4%)	0	100	100
36	W	129/236 (55%)	126 (98%)	3 (2%)	0	100	100
37	X	118/142 (83%)	114 (97%)	4 (3%)	0	100	100
38	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
39	y	223/245 (91%)	211 (95%)	12 (5%)	0	100	100
40	Z	133/136 (98%)	117 (88%)	16 (12%)	0	100	100
41	z	53/106 (50%)	53 (100%)	0	0	100	100
42	D	245/297 (82%)	225 (92%)	17 (7%)	3 (1%)	11	43
43	J	162/174 (93%)	141 (87%)	17 (10%)	4 (2%)	4	29
44	q	95/106 (90%)	76 (80%)	18 (19%)	1 (1%)	12	45
45	o	52/59 (88%)	48 (92%)	4 (8%)	0	100	100
All	All	6774/8171 (83%)	6248 (92%)	495 (7%)	31 (0%)	27	59

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	339	LEU
27	u	3	ILE
43	J	95	ASN
16	I	17	ASP
22	L	63	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	v	309/467 (66%)	304 (98%)	5 (2%)	58	76
3	A	188/196 (96%)	187 (100%)	1 (0%)	86	93
4	a	77/119 (65%)	75 (97%)	2 (3%)	41	65
5	B	322/323 (100%)	318 (99%)	4 (1%)	67	82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	b	211/573 (37%)	205 (97%)	6 (3%)	38	64
7	C	288/289 (100%)	286 (99%)	2 (1%)	81	90
8	c	81/88 (92%)	78 (96%)	3 (4%)	29	58
9	d	94/97 (97%)	94 (100%)	0	100	100
10	E	137/153 (90%)	134 (98%)	3 (2%)	47	69
11	e	109/111 (98%)	107 (98%)	2 (2%)	54	74
12	F	186/205 (91%)	185 (100%)	1 (0%)	86	93
13	f	90/91 (99%)	90 (100%)	0	100	100
14	G	189/208 (91%)	185 (98%)	4 (2%)	48	71
15	g	95/103 (92%)	95 (100%)	0	100	100
16	I	116/141 (82%)	115 (99%)	1 (1%)	75	87
17	H	168/171 (98%)	166 (99%)	2 (1%)	67	82
18	h	104/105 (99%)	104 (100%)	0	100	100
19	i	78/82 (95%)	78 (100%)	0	100	100
20	j	69/71 (97%)	68 (99%)	1 (1%)	62	79
21	k	68/69 (99%)	68 (100%)	0	100	100
22	L	147/159 (92%)	141 (96%)	6 (4%)	26	55
23	l	45/46 (98%)	43 (96%)	2 (4%)	24	53
24	M	108/109 (99%)	107 (99%)	1 (1%)	75	87
25	p	71/72 (99%)	70 (99%)	1 (1%)	62	79
26	N	175/176 (99%)	173 (99%)	2 (1%)	70	83
27	u	132/180 (73%)	128 (97%)	4 (3%)	36	63
28	O	160/162 (99%)	157 (98%)	3 (2%)	52	73
29	P	143/146 (98%)	141 (99%)	2 (1%)	62	79
30	Q	126/151 (83%)	125 (99%)	1 (1%)	79	88
31	R	127/154 (82%)	126 (99%)	1 (1%)	79	88
32	S	154/156 (99%)	153 (99%)	1 (1%)	84	92
33	T	50/137 (36%)	47 (94%)	3 (6%)	16	45
34	U	91/107 (85%)	89 (98%)	2 (2%)	47	69
35	V	104/105 (99%)	104 (100%)	0	100	100
36	W	113/213 (53%)	111 (98%)	2 (2%)	54	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	X	104/118 (88%)	103 (99%)	1 (1%)	73	85
38	Y	109/110 (99%)	109 (100%)	0	100	100
39	y	192/211 (91%)	192 (100%)	0	100	100
40	Z	115/116 (99%)	114 (99%)	1 (1%)	75	87
41	z	48/95 (50%)	48 (100%)	0	100	100
42	D	203/245 (83%)	199 (98%)	4 (2%)	50	72
43	J	140/150 (93%)	139 (99%)	1 (1%)	81	90
44	q	84/91 (92%)	83 (99%)	1 (1%)	67	82
45	o	43/47 (92%)	42 (98%)	1 (2%)	45	68
All	All	5763/6918 (83%)	5686 (99%)	77 (1%)	64	81

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	P	97	ASN
42	D	39	GLN
31	R	98	ARG
34	U	94	ARG
44	q	88	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
34	U	49	ASN
43	J	95	ASN
35	V	98	ASN
39	y	106	ASN
44	q	82	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	1	3198/3396 (94%)	722 (22%)	39 (1%)
47	2	120/121 (99%)	15 (12%)	0
48	3	156/158 (98%)	28 (17%)	2 (1%)
All	All	3474/3675 (94%)	765 (22%)	41 (1%)

5 of 765 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	1	22	G
46	1	40	A
46	1	43	A
46	1	44	U
46	1	45	A

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	1	2513	U
46	1	3218	A
46	1	2537	U
46	1	2769	A
46	1	3269	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

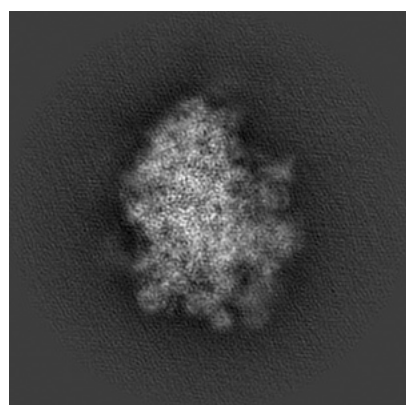
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0371. These allow visual inspection of the internal detail of the map and identification of artifacts.

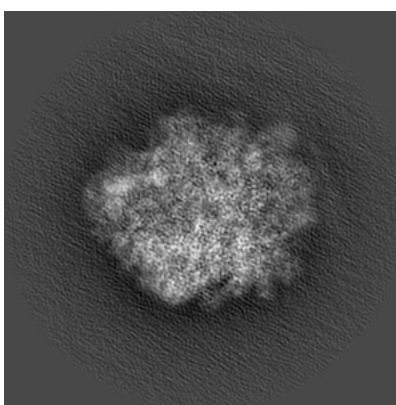
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

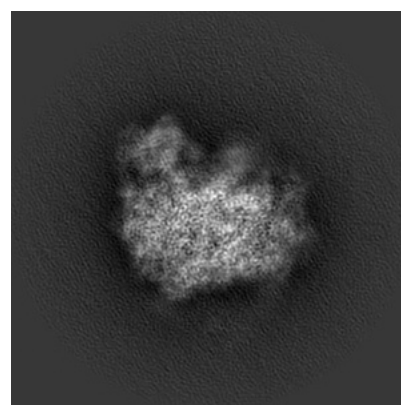
6.1.1 Primary map



X



Y

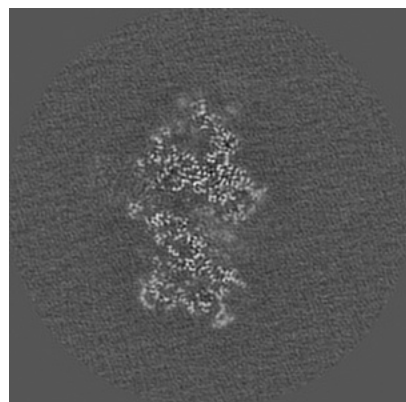


Z

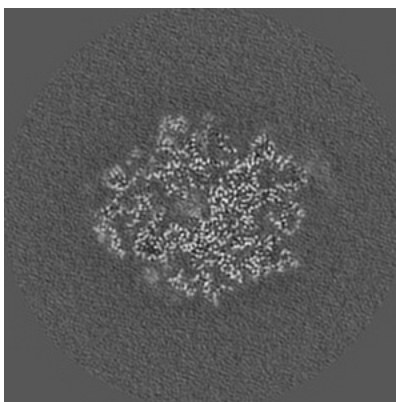
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

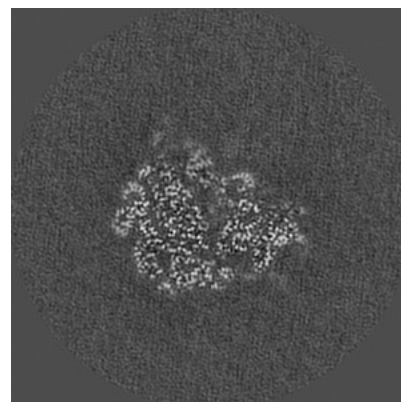
6.2.1 Primary map



X Index: 192



Y Index: 192

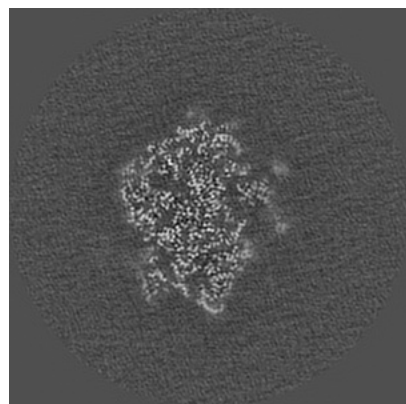


Z Index: 192

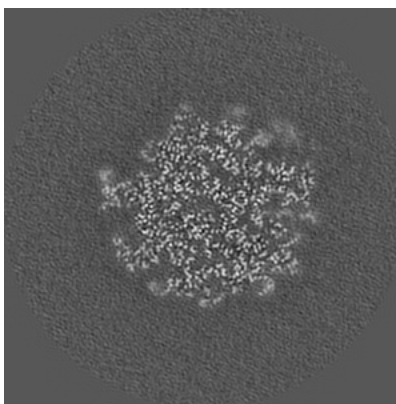
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

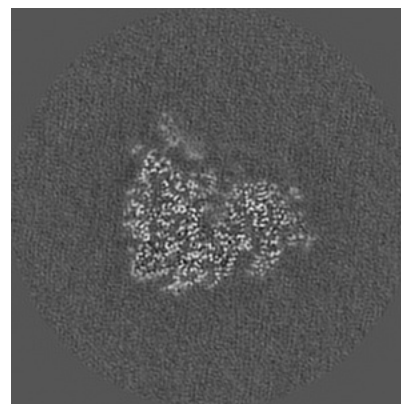
6.3.1 Primary map



X Index: 166



Y Index: 173

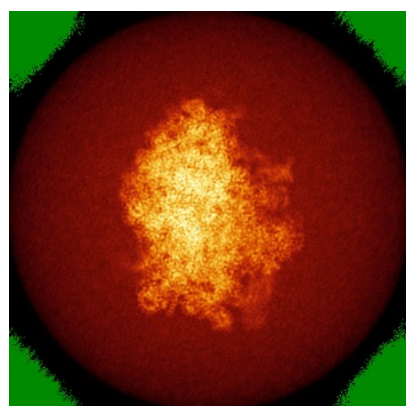


Z Index: 184

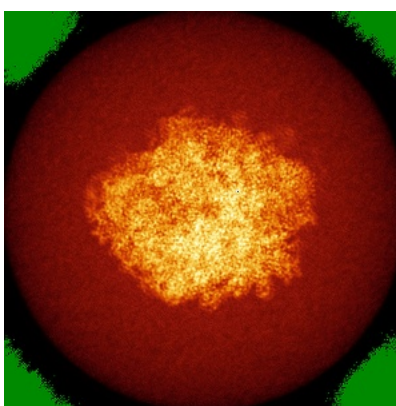
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

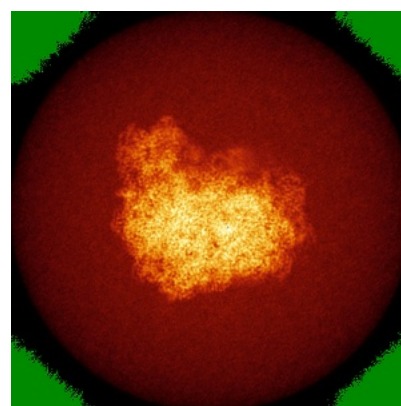
6.4.1 Primary map



X



Y

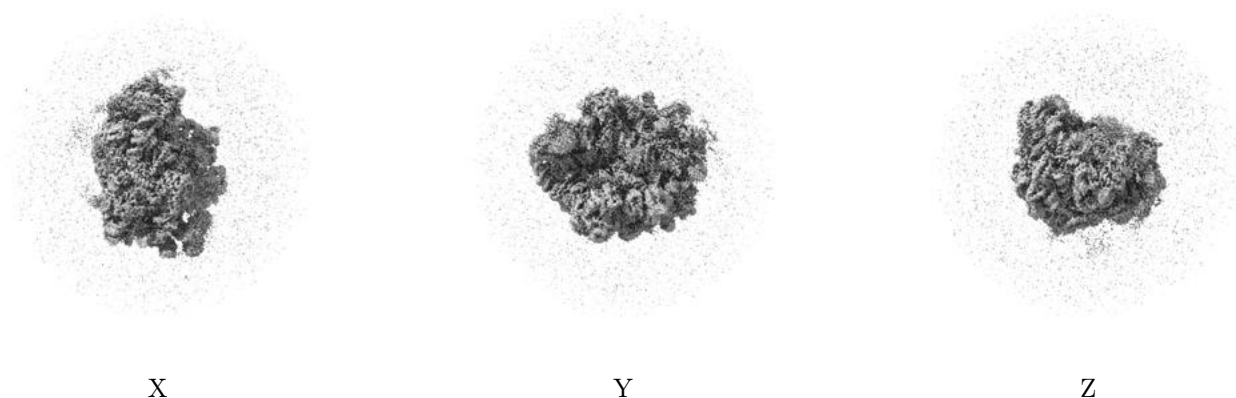


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

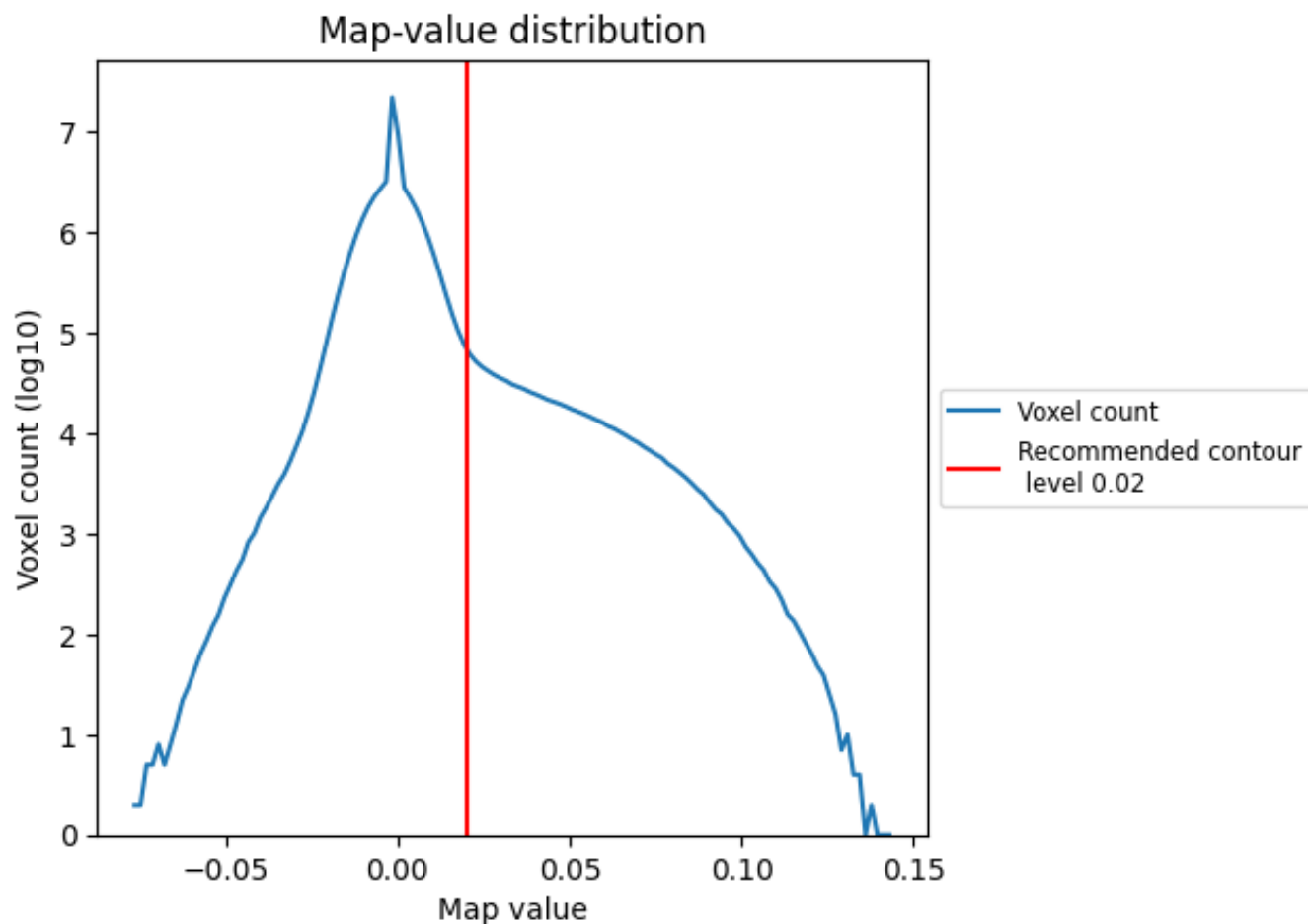
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

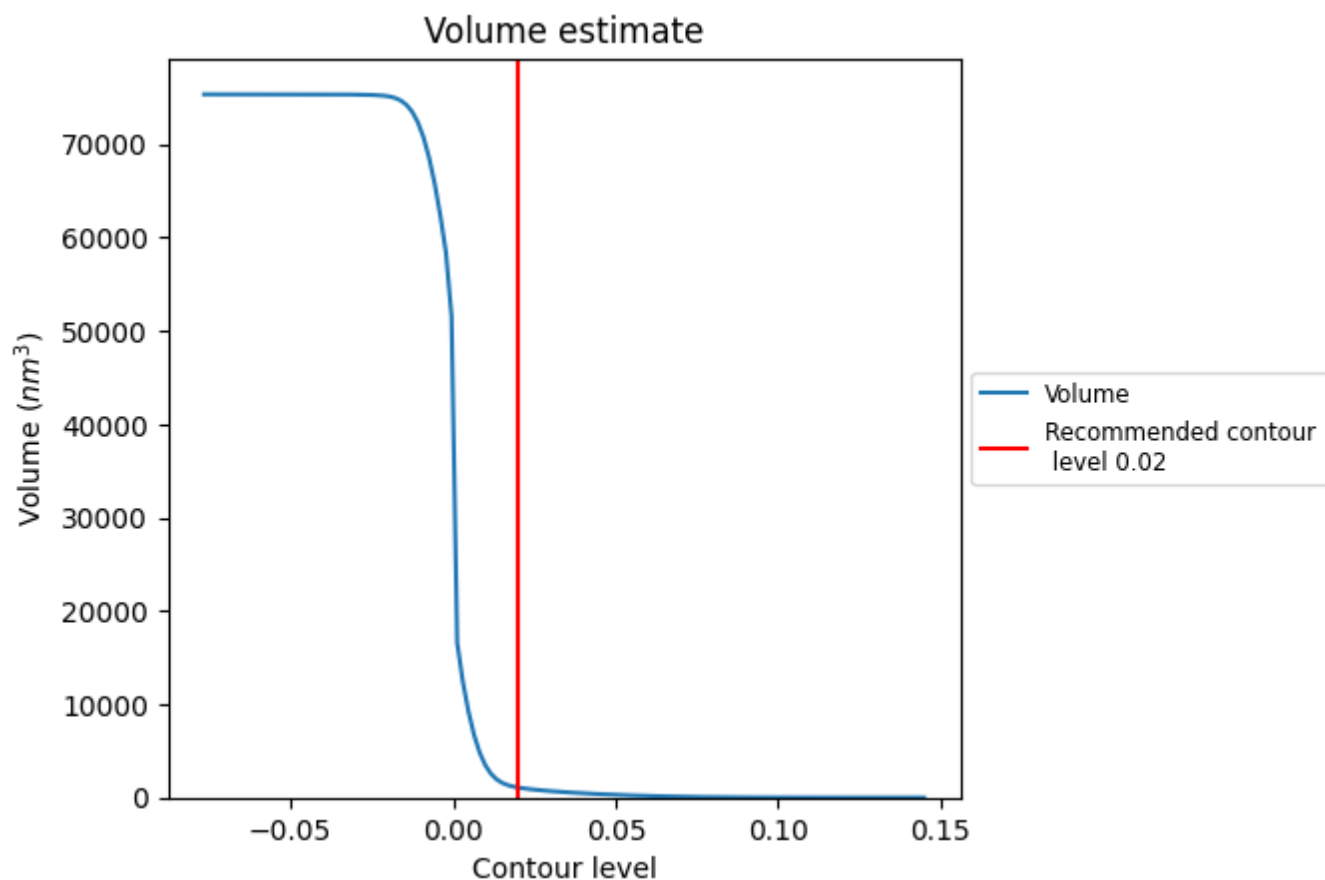
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

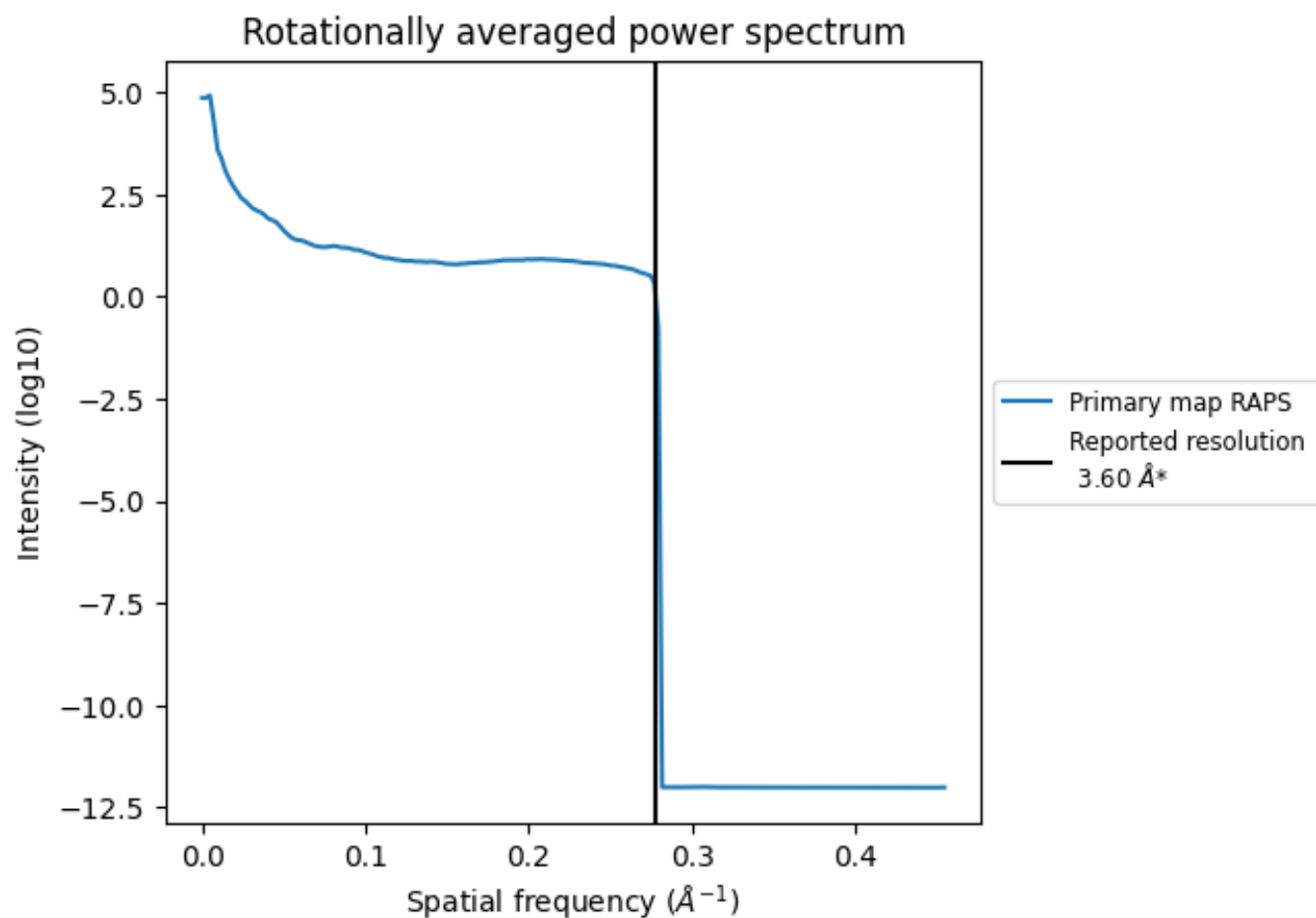
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1076 nm³; this corresponds to an approximate mass of 972 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

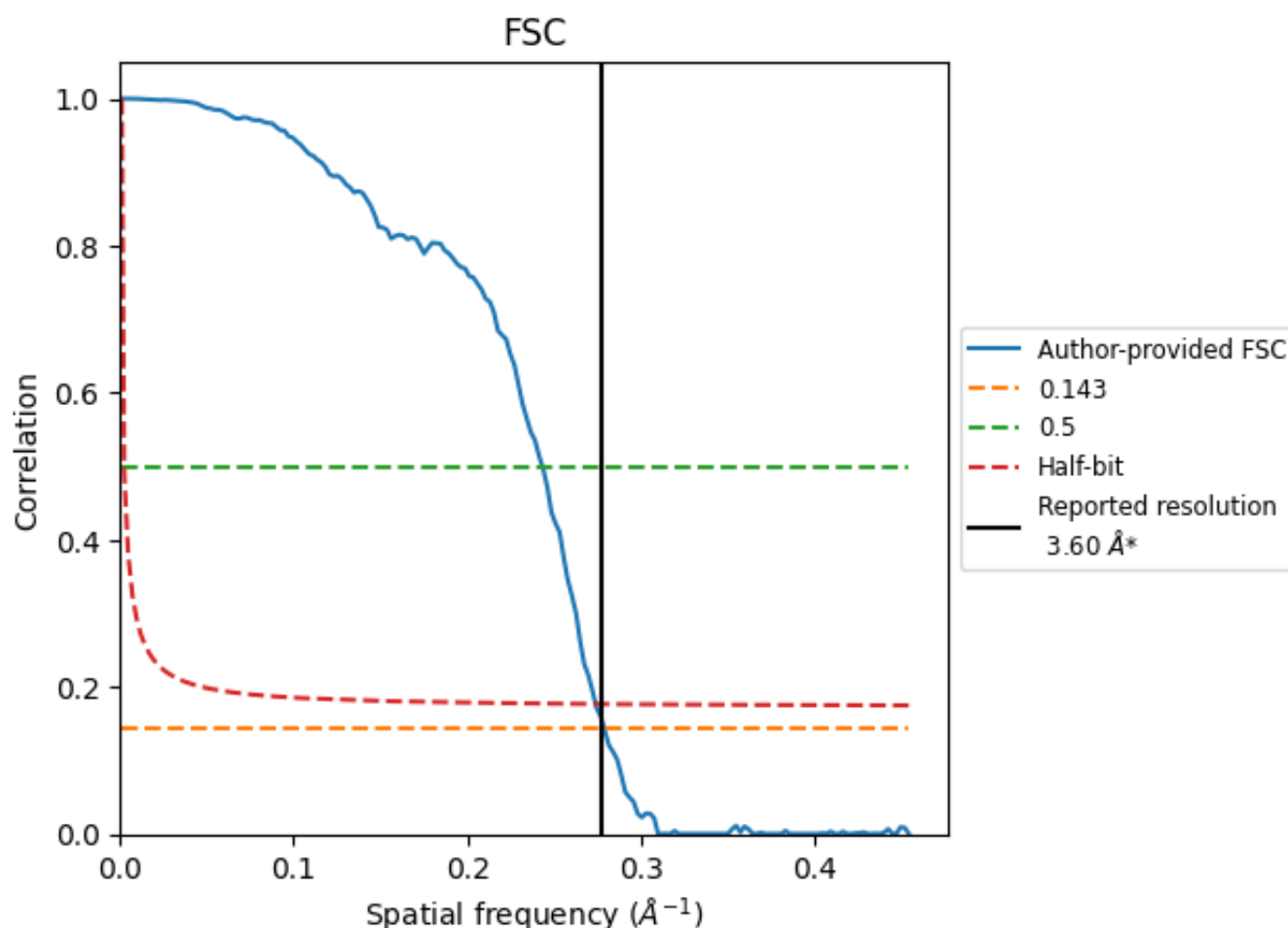


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

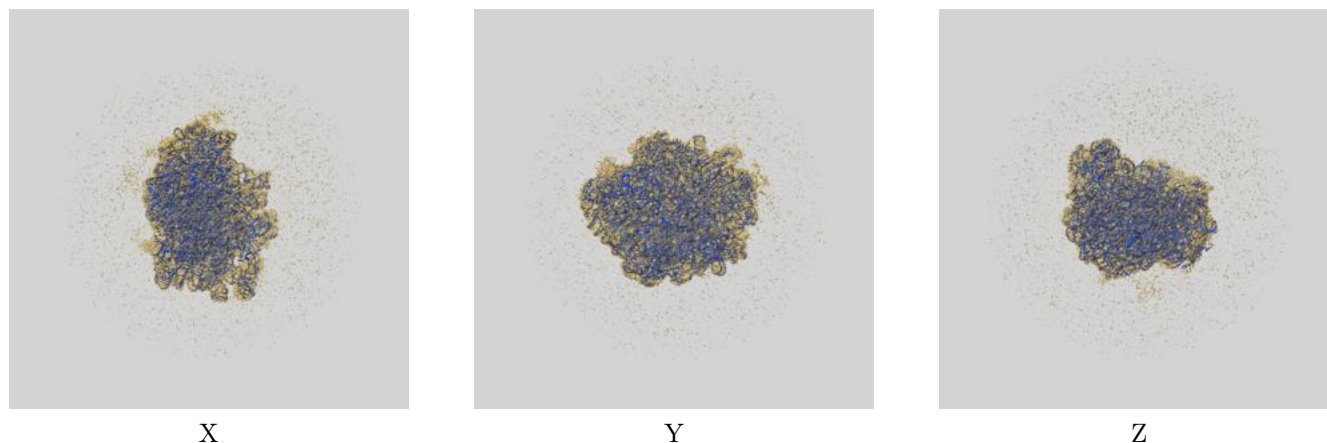
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.58	4.11	3.65
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

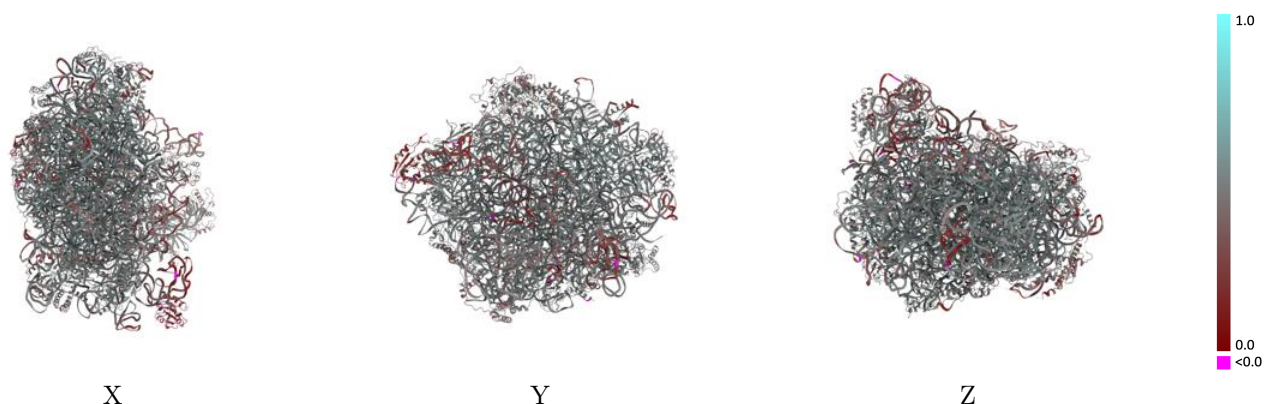
This section contains information regarding the fit between EMDB map EMD-0371 and PDB model 6N8L. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



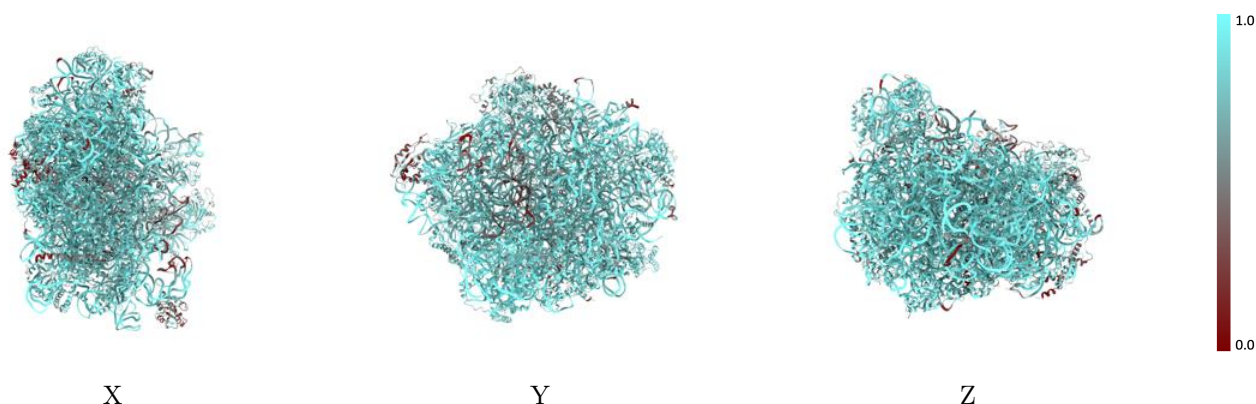
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



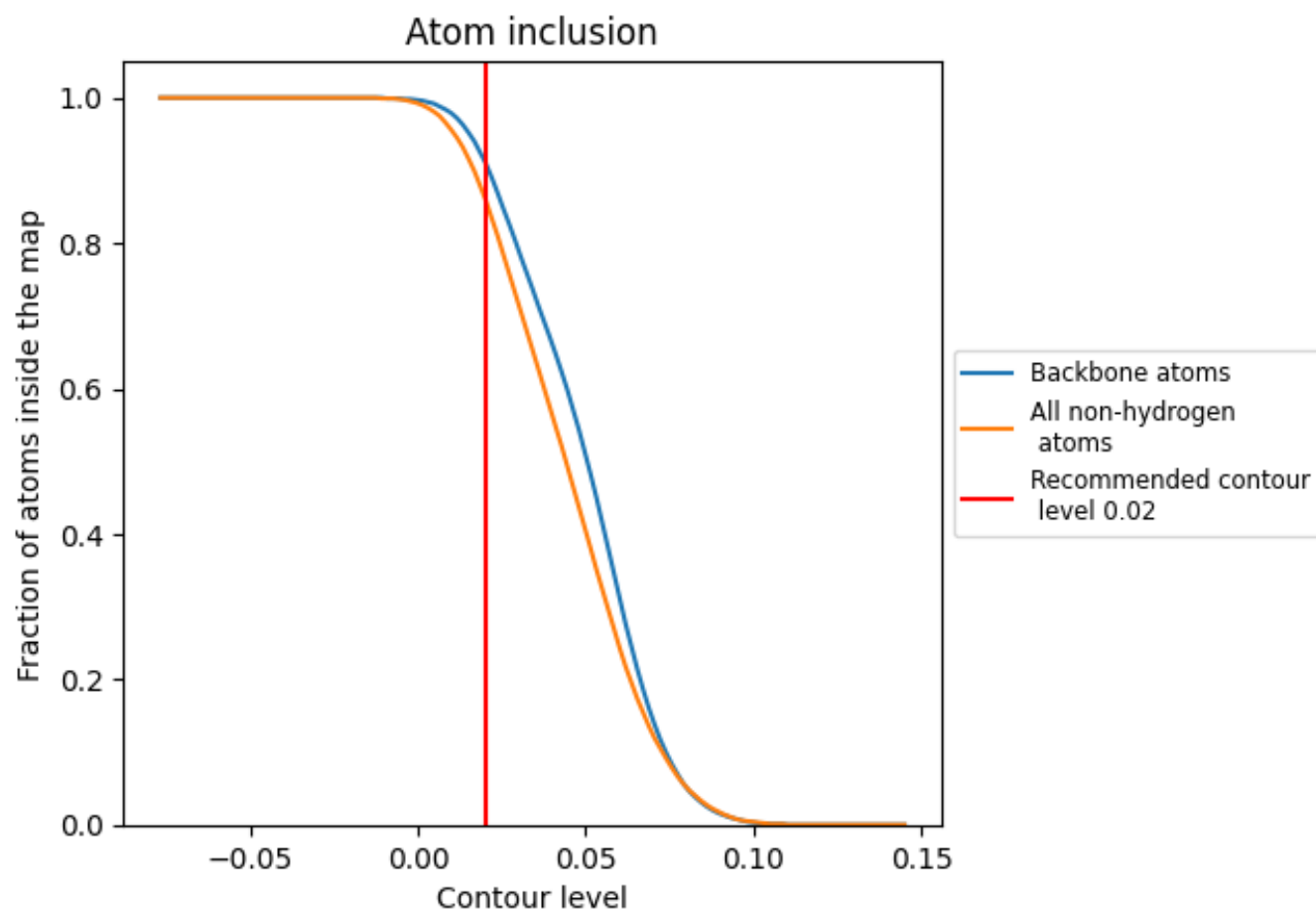
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





























The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8620	 0.4720
1	 0.9180	 0.4740
2	 0.9620	 0.4790
3	 0.9550	 0.4970
A	 0.8590	 0.5240
B	 0.8510	 0.5050
C	 0.8370	 0.5050
D	 0.8250	 0.4450
E	 0.7980	 0.4730
F	 0.8380	 0.4930
G	 0.8300	 0.4780
H	 0.8310	 0.4790
I	 0.5740	 0.4450
J	 0.7510	 0.4120
L	 0.8500	 0.4950
M	 0.8370	 0.4800
N	 0.8690	 0.5260
O	 0.8530	 0.5110
P	 0.8240	 0.5010
Q	 0.8530	 0.5040
R	 0.8390	 0.4980
S	 0.8210	 0.4960
T	 0.7750	 0.4230
U	 0.7800	 0.4170
V	 0.7960	 0.5020
W	 0.4710	 0.2330
X	 0.8360	 0.5020
Y	 0.8450	 0.5010
Z	 0.8270	 0.4950
a	 0.8420	 0.4950
b	 0.3890	 0.3710
c	 0.8250	 0.4680
d	 0.8280	 0.5000
e	 0.8260	 0.5170
f	 0.8540	 0.5260



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.7970	 0.5000
h	 0.8320	 0.4920
i	 0.8430	 0.4850
j	 0.8870	 0.5350
k	 0.7600	 0.4660
l	 0.8530	 0.5220
o	 0.7990	 0.4720
p	 0.8190	 0.5090
q	 0.4150	 0.1540
s	 0.8420	 0.4070
u	 0.6980	 0.4340
v	 0.6310	 0.4180
y	 0.7810	 0.4540
z	 0.4170	 0.3790